

SEQUENCE LISTING

<110> REGENTS OF THE UNIVERSITY OF CALIFORNIA
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 TING, Alice
 ZHANG, Jin

<120> EMISSION RATIONOMETRIC INDICATORS OF PHOSPHORYLATION

<130> REGEN1550

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<170> PatentIn version 3.0

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<211> 716

<212> DNA

<213> Aequorea victoria

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 Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

ggt gaa ggt gat gca aca tac gga aaa ctt acc ctt aaa ttt att tgc 144
 Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

act act gga aaa cta cct gtt cca tgg cca aca ctt gtc act act ttc 192
 Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

tct tat ggt gtt caa tgc ttt tca aga tac cca gat cat atg aaa cag 240
 Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

cat gac ttt ttc aag agt gcc atg ccc gaa ggt tat gta cag gaa aga 288
 His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

act ata ttt ttc aaa gat gac ggg aac tac aag aca cgt gct gaa gtc 336
 Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

aag ttt gaa ggt gat acc ctt gtt aat aga atc gag tta aaa ggt att 384
 Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
 115 120 125

gat ttt aaa gaa gat gga aac att ctt gga cac aaa ttg gaa tac aac 432
 Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

09865291.052401
 T07250.F0259960

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 Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly 160
 145 150 155

atc aaa gtt aac ttc aaa att aga cac aac att gaa gat gga agc gtt 528
 Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val 175
 165 170

caa cta gca gac cat tat caa caa aat act cca att ggc gat ggc cct 576
 Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro 190
 180 185

gtc ctt tta cca gac aac cat tac ctg tcc aca caa tct gcc ctt tcg 624
 Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser 205
 195 200

aaa gat ccc aac gaa aag aga gac cac atg gtc ctt ctt gag ttt gta 672
 Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val 220
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 <212> PRT
 <213> Aequorea victoria
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Met Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
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Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
 20 25 30

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
 35 40 45

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
 50 55 60

Ser Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln
 65 70 75 80

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
 85 90 95

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
 100 105 110

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile

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115

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Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
 130 135 140

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly
 145 150 155 160

Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val
 165 170 175

Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro
 180 185 190

Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser
 195 200 205

Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val
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Thr Ala Ala Gly Ile Thr His Gly Met Asp Glu Leu Tyr Lys
 225 230 235

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 20 25 30

gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
 Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
 Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

ctg acc tac ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
 Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
 65 70 75 80

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 85 90 95
 cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
 Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110
 gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
 Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125
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 Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140
 aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160
 ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175
 gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190
 ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
 195 200 205
 agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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<210> 4
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Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu
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Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr

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Leu Thr Tyr Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
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Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

ctg acc tgg ggc gtg cag tgc ttc agc cgc tac ccc gac cac atg aag 240
Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

cgt acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

aac tac atc agc cac aac gtc tat atc acc gcc gac aag cag aag aac 480
Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

ggc atc aag gcc cac ttc aag atc cgc cac aac atc gag gac ggc agc 528
Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc acc cag tcc gcc ctg 624
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa 720
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T04250 T625960

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20 25 30

Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
210 215 220

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

gtg acc gcc gcc ggg atc act ctc ggc atg gac gag ctg tac aag taa 720
 Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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 <212> PRT
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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Val Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
 115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
 130 135 140

Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

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Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
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Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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gtc gag ctg gac ggc gac gta aac ggc cac aag ttc agc gtg tcc ggc 96
Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly
20 25 30
gag ggc gag ggc gat gcc acc tac ggc aag ctg acc ctg aag ttc atc 144
Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45
tgc acc acc ggc aag ctg ccc gtg ccc tgg ccc acc ctc gtg acc acc 192
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60
ttc ggc tac ggc ctg aag tgc ttc gcc cgc tac ccc gac cac atg aag 240
Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
65 70 75 80
cag cac gac ttc ttc aag tcc gcc atg ccc gaa ggc tac gtc cag gag 288
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95
cgc acc atc ttc ttc aag gac gac ggc aac tac aag acc cgc gcc gag 336
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110
gtg aag ttc gag ggc gac acc ctg gtg aac cgc atc gag ctg aag ggc 384
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125
atc gac ttc aag gag gac ggc aac atc ctg ggg cac aag ctg gag tac 432

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Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
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aac tac aac agc cac aac gtc tat atc atg gcc gac aag cag aag aac 480
 Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn
 145 150 155 160

ggc atc aag gtg aac ttc aag atc cgc cac aac atc gag gac ggc agc 528
 Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
 165 170 175

gtg cag ctc gcc gac cac tac cag cag aac acc ccc atc ggc gac ggc 576
 Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
 180 185 190

ccc gtg ctg ctg ccc gac aac cac tac ctg agc tac cag tcc gcc ctg 624
 Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 195 200 205

agc aaa gac ccc aac gag aag cgc gat cac atg gtc ctg ctg gag ttc 672
 Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 210 215 220

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<210> 10
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 <213> Aequorea victoria

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 35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
 50 55 60

Phe Gly Tyr Gly Leu Lys Cys Phe Ala Arg Tyr Pro Asp His Met Lys
 65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
 85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
 100 105 110

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 cag tat gga agc aag gta tat gtc aag cac cct gcc gac ata cca gac 296
 Gln Tyr Gly Ser Lys Val Tyr Val Lys His Pro Ala Asp Ile Pro Asp
 70 75 80
 tat aaa aag ctg tca ttt cct gaa gga ttt aaa tgg gaa agg gtc atg 344
 Tyr Lys Lys Leu Ser Phe Pro Glu Gly Phe Lys Trp Glu Arg Val Met
 85 90 95
 aac ttt gaa gac ggt ggc gtc gtt act gta acc cag gat tcc agt ttg 392
 Asn Phe Glu Asp Gly Gly Val Val Thr Val Thr Gln Asp Ser Ser Leu
 100 105 110
 cag gat ggc tgt ttc atc tac aag gtc aag ttc att ggc gtg aac ttt 440
 Gln Asp Gly Cys Phe Ile Tyr Lys Val Lys Phe Ile Gly Val Asn Phe
 115 120 125
 cct tcc gat gga cct gtt atg caa aag aag aca atg ggc tgg gaa gcc 488
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 130 135 140 145
 agc act gag cgt ttg tat cct cgt gat ggc gtg ttg aaa gga gag att 536
 Ser Thr Glu Arg Leu Tyr Pro Arg Asp Gly Val Leu Lys Gly Glu Ile
 150 155 160
 cat aag gct ctg aag ctg aaa gac ggt ggt cat tac cta gtt gaa ttc 584
 His Lys Ala Leu Lys Leu Lys Asp Gly Gly His Tyr Leu Val Glu Phe
 165 170 175
 aaa agt att tac atg gca aag aag cct gtg cag cta cca ggg tac tac 632
 Lys Ser Ile Tyr Met Ala Lys Lys Pro Val Gln Leu Pro Gly Tyr Tyr
 180 185 190
 tat gtt gac tcc aaa ctg gat ata aca agc cac aac gaa gac tat aca 680
 Tyr Val Asp Ser Lys Leu Asp Ile Thr Ser His Asn Glu Asp Tyr Thr
 195 200 205
 atc gtt gag cag tat gaa aga acc gag gga cgc cac cat ctg ttc ctt 728
 Ile Val Glu Gln Tyr Glu Arg Thr Glu Gly Arg His His Leu Phe Leu
 210 215 220 225
 taa ggctgaactt ggctcagacg tgggtgagcg gtaatgacca caaaaggcag 781
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<210> 12
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<213> Artificial sequence
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<210> 14
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<223> Xaa is any Amino Acid

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<223> Synthetic peptide

<400> 19

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<211> 7

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<400> 20

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Leu Arg Arg Ala Ser Leu Pro
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1 5

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Gly Ser His Ser Gly Ser Gly Lys Pro
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0985291.052401
T07250 T6259860

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<400> 25

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<220>
 <223> Reverse primer for PCR

<400> 27 60
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 92
 cgccctgcaga gtctgatgtc caaagtgtta gg

<210> 28
 <211> 33
 <212> DNA
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<220>
 <223> Primer for PCR

<400> 28 33
 cgccgcgccca gcctgccagg caccggcggc agc

<210> 29
 <211> 33
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Primer for PCR

<400> 29 33
 gctgccgccg gtggctggca ggctggcgcg acg

<210> 30
 <211> 32
 <212> DNA

0986591.05401
 T04250" T6259860

<213> Artificial sequence

<220>

<223> Primer for PCR

<400> 30

gcctccgtcg cgccgcactg ccaggcaccg gc

32

<210> 31

<211> 32

<212> DNA

<213> Artificial sequence

<220>

<223> Primer for PCR

<400> 31

gccgggtgcct ggcagtgcg cgcgacggag gc

32

<210> 32

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<400> 32

Leu Arg Arg Ala Ser Leu Gly
1 5

<210> 33

<211> 9

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<400> 33

Ala Gln Arg Ser Thr Ser Thr Pro Asn
1 5

<210> 34

<211> 6

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (1)..(6)

<223> Xaa is any Animo Acid

0985241 052401
T04250" T0259360

<400> 34

Arg Ser Xaa Ser Xaa Pro
1 5

<210> 35
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<220>
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<400> 35

Arg Arg Xaa Ser
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<210> 36
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<213> Artificial sequence

<220>
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<220>
<221> VARIANT
<222> (2)..(3)
<223> Xaa is any Amino Acid

<220>
<221> VARIANT
<222> (4)..(4)
<223> Xaa is Serine or Threonine

<400> 36

Arg Xaa Xaa Xaa
1

<210> 37
<211> 4
<212> PRT
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<220>
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<220>
<221> VARIANT
<222> (1)..(1)
<223> Xaa is Lysine or Arginine

0965291 052404
T04250 T6259860

<220>
 <221> VARIANT
 <222> (2)..(3)
 <223> Xaa is any Amino Acid

<220>
 <221> VARIANT
 <222> (4)..(4)
 <223> Xaa is Serine or Threonine

<400> 37

Xaa Xaa Xaa Xaa
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<210> 38
 <211> 39
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Forward primer for PCR

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39

<210> 39
 <211> 99
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<220>
 <223> Reverse primer for PCR

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agatccagag tgagacccca cgggttgctc taggcacag

99

<210> 40
 <211> 35
 <212> DNA
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<220>
 <223> Forward primer for PCR

<400> 40
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35

<210> 41
 <211> 93
 <212> DNA
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0985591.052401
 104250.16259860

<220>

<223> Reverse primer for PCR

<400> 41

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tccagatgta gaccacaga cgtagtcag gcg 93

<210> 42

<211> 7

<212> PRT

<213> Artificial sequence

<220>

<223> Synthetic peptide

<220>

<221> VARIANT

<222> (2)..(2)

<223> Xaa is Arginine or Lysine

<220>

<221> VARIANT

<222> (3)..(3)

<223> Xaa is Phenylalanine, Arginine, Serine or Asparagine

<220>

<221> VARIANT

<222> (4)..(4)

<223> Xaa is Arginine, Histidine, Lysine

<220>

<221> VARIANT

<222> (5)..(5)

<223> Phosphorylated peptide

<220>

<221> VARIANT

<222> (6)..(6)

<223> Xaa is Tryptophan, Tyrosine, Phenylalanine, Leucine

<400> 42

Arg Xaa Xaa Xaa Ser Xaa Pro

1

5

T04250-16259560